

SEQUENCE LISTING

<110> Croteau, Rodney B
Bohlmann, Joerg
Steele, Christopher L
Phillips, Michael A

<120> MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

<130> WSUR18414

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<150> 09/360,545

<151> 1999-07-26

<150> 60/052,249

<151> 1997-07-11

<150> PCT/US98/14528

<151> 1998-07-10

<160> 107

<170> PatentIn Ver. 2.0

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<223> Clone AG2.2 encoding myrcene synthase

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SEQUENCE LISTING

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Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
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Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
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Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
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Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
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Glu 335	Met 340	Thr 345	Phe 350	Cys 355	Arg 360	His 365	Arg 370	His 375	Val 380	Glu 385	Tyr 390	Tyr 395	Thr 400	Leu 405
Ser 350	Cys 355	Ile 360	Ala 365	Phe 370	Glu 375	Pro 380	Gln 385	His 390	Ser 395	Gly 400	Phe 405	Arg 410	Leu 415	Gly 420
Ala 365	Lys 370	Thr 375	Cys 380	His 385	Leu 390	Ile 395	Thr 400	Val 405	Leu 410	Asp 415	Asp 420	Met 425	Tyr 430	Asp 435
Phe 385	Gly 390	Thr 395	Val 400	Asp 405	Glu 410	Leu 415	Glu 420	Leu 425	Phe 430	Thr 435	Ala 440	Thr 445	Met 450	Lys 455
Trp 400	Asp 405	Pro 410	Ser 415	Ser 420	Ile 425	Asp 430	Cys 435	Leu 440	Pro 445	Glu 450	Tyr 455	Met 460	Lys 465	Gly 470
Tyr 415	Ile 420	Ala 425	Val 430	Tyr 435	Asp 440	Thr 445	Val 450	Asn 455	Glu 460	Met 465	Ala 470	Arg 475	Glu 480	Ala 485
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Tyr 465	Leu 470	Pro 475	Ser 480	Phe 485	Asp 490	Glu 495	Tyr 500	Tyr 505	Glu 510	Asn 515	Gly 520	Lys 525	Val 530	Ser 535
Gly 480	His 485	Arg 490	Ile 495	Ser 500	Ala 505	Leu 510	Gln 515	Pro 520	Ile 525	Leu 530	Thr 535	Met 540	Asp 545	Ile 550

Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn
500 505 510

Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
515 520 525

Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
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Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile
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Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp
580 585 590

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Met Ala Leu Leu Ser Ile Val Ser Leu Gln Val Pro Lys
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tcc tgc ggg ctg aaa tcg ttg atc agt tcc agc aat gtg cag aag gct 159

Ser Cys Gly Leu Lys Ser Leu Ile Ser Ser Ser Asn Val Gln Lys Ala
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ctc tgt atc tct aca gca gtc cca aca ctc aga atg cgt agg cga cag 207

Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln
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aaa gct ctg gtc atc aac atg aaa ttg acc act gta tcc cat cgt gat 255

Lys Ala Leu Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp
50 55 60

gat aat ggt ggt ggt gta ctg caa aga cgc ata gcc gat cat cat ccc 303

Asp Asn Gly Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro
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Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln	
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tct atc tcc aga tgg tgg aaa gaa tca ggt tcg tct caa ctg act ttt	1119
Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe	
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aca cgg cat cgt cac gtg gaa tac tac act atg gca tct tgc att tct	1167
Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser	
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atg ttg cca aaa cat tca gct ttc aga atg gag ttt gtc aaa gtg tgt	1215
Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys	
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cat ctt gta aca gtt ctc gat gat ata tat gac act ttt gga aca atg	1263
His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met	
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Asn Glu Leu Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser	
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acg aca agg tgg ctt cca gaa tat atg aaa gga gtg tac atg gac ttg	1359
Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu	
415 420 425	
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Tyr Gln Cys Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly	
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Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp	
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acc ttt atg caa gaa gca aag tgg atc tcc agc agt tat ctc cca acg	1503
Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr	
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Phe Glu Glu Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile	
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Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr	
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ata ctg caa gaa att gat tat cca tcc aga ttc aat gag tta gct tcg	1647
Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser	
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Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His	
545 550 555	
cct gga tca ata gag gaa gat gct ctc aat cat atc aac gcc atg atc	1791

Pro	Gly	Ser	Ile	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile	Asn	Ala	Met	Ile	
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Ser	Asp	Ala	Ile	Arg	Glu	Leu	Asn	Trp	Glu	Leu	Leu	Arg	Pro	Asp	Ser	
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Lys	Ser	Pro	Ile	Ser	Ser	Lys	Lys	His	Ala	Phe	Asp	Ile	Thr	Arg	Ala	
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Phe	His	His	Val	Tyr	Lys	Tyr	Arg	Asp	Gly	Tyr	Thr	Val	Ser	Asn	Asn	
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Glu	Thr	Lys	Asn	Leu	Val	Met	Lys	Thr	Val	Leu	Glu	Pro	Leu	Ala	Leu	
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Ser	Thr	Ala	Val	Pro	Thr	Leu	Arg	Met	Arg	Arg	Arg	Gln	Lys	Ala	Leu	
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Val	Ile	Asn	Met	Lys	Leu	Thr	Thr	Val	Ser	His	Arg	Asp	Asp	Asn	Gly	
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Glu	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ser	Ser	Pro	Tyr	Gly	Gly	Ser	Ser	
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Asn	Ser	Ile	Pro	Asn	Asn	Arg	Glu	Leu	Phe	Gly	Ser	Gln	Asn	Asp	Leu	
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Leu	Thr	Arg	Leu	Trp	Met	Val	Asp	Ser	Ile	Glu	Arg	Leu	Gly	Ile	Asp	
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Arg	His	Phe	Gln	Asn	Glu	Ile	Arg	Val	Ala	Leu	Asp	Tyr	Val	Tyr	Ser	
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Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
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 Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
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 Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Glu Lys
 195 200 205
 Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
 210 215 220
 Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu
 225 230 235 240
 Lys Val Met Glu Glu Ala Glu Ile Phe Ser Ala Ser Tyr Leu Lys Lys
 245 250 255
 Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu Ile Glu Tyr
 260 265 270
 Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg
 275 280 285
 Asn Tyr Ile Glu Val Tyr Glu Gln Ser Gly Tyr Glu Ser Leu Asn Glu
 290 295 300
 Met Pro Tyr Met Asn Met Lys Lys Leu Leu Gln Leu Ala Lys Leu Glu
 305 310 315 320
 Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln Ser Ile Ser
 325 330 335
 Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe Thr Arg His
 340 345 350
 Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser Met Leu Pro
 355 360 365
 Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys His Leu Val
 370 375 380
 Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met Asn Glu Leu
 385 390 395 400
 Gln Leu Phe Thr Asp Ala Ile Lys Arg Trp Asp Leu Ser Thr Thr Arg
 405 410 415
 Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu Tyr Gln Cys
 420 425 430
 Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly Arg Asp Met
 435 440 445
 Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp Thr Phe Met
 450 455 460
 Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr Phe Glu Glu
 465 470 475 480
 Tyr Leu Lys Asn Ala Lys Val Ser Ser Gly Ser Arg Ile Ala Thr Leu

485

490

495

Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr Ile Leu Gln
500 505 510

Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser Ser Ile Leu
515 520 525

Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Ala Arg Gly
530 535 540

Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His Pro Gly Ser
545 550 555 560

Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
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tac aga gaa cgc gcg gag gtc ctt gtt agc gag att aaa gtg atg ctt 97
Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu
20 25 30

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Tyr	Asp	Thr	Ala	Trp	Val	Ala	Arg	Val	Pro	Ala	Ile	Asp	Gly	Ser	Ala	
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cgc	ccg	caa	ttt	ccc	caa	aca	gtt	gac	tgg	att	ttg	aaa	aac	cag	tta	241
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Lys	Asp	Gly	Ser	Trp	Gly	Ile	Gln	Ser	His	Phe	Leu	Leu	Ser	Asp	Arg	
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Cys	Leu	Tyr	Pro	Val	Asp	Leu	Leu	Glu	Arg	Leu	Leu	Ile	Val	Asp	Asn	
260265270																
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Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu	
275 280 285	
gct ctt gat tat gtt tac agg cat tgg aac gaa aga gga att ggg tgg	913
Ala Leu Asp Tyr Val Tyr Arg His Trp Asn Glu Arg Gly Ile Gly Trp	
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Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe	
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cga ttg ctt cgg ctg cat agg tac aat gta tct cca gcc att ttt gac	1009
Arg Leu Leu Arg Leu His Arg Tyr Asn Val Ser Pro Ala Ile Phe Asp	
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Asn Phe Lys Asp Ala Asn Gly Lys Phe Ile Cys Ser Thr Gly Gln Phe	
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Asn Lys Asp Val Ala Ser Met Leu Asn Leu Tyr Arg Ala Ser Gln Leu	
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Ala Phe Pro Gly Glu Asn Ile Leu Asp Glu Ala Lys Ser Phe Ala Thr	
370 375 380	
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Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp	
385 390 395 400	
aac aac aaa caa aac ctg agc caa gag atc aaa tac gcg ctg aag act	1249
Asn Asn Lys Gln Asn Leu Ser Gln Glu Ile Lys Tyr Ala Leu Lys Thr	
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Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln	
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Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu	
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Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe	
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Asn Ile Ile Gln Ser Ile His Gln Glu Met Lys Asn Val Thr Ser	
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Trp Phe Arg Asp Ser Gly Leu Pro Leu Phe Thr Phe Ala Arg Glu Arg	
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Pro Leu Glu Phe Tyr Phe Leu Val Ala Ala Gly Thr Tyr Glu Pro Gln	
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Glu	Ala	Glu	Trp	Leu	Ala	Ala	Glu	Tyr	Val	Pro	Thr	Leu	Asp	Glu	Tyr		
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Arg	Gly	Glu	Leu	Ala	Ser	Ser	Ile	Glu	Cys	Tyr	Met	Lys	Asp	His	Pro		
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Glu	Cys	Thr	Glu	Glu	Glu	Ala	Leu	Asp	His	Ile	Tyr	Ser	Ile	Leu	Glu		
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Pro	Ala	Val	Lys	Glu	Leu	Thr	Arg	Glu	Phe	Leu	Lys	Pro	Asp	Asp	Val		
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Pro	Phe	Ala	Cys	Lys	Lys	Met	Leu	Phe	Glu	Glu	Thr	Arg	Val	Thr	Met		
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Val	Ile	Phe	Lys	Asp	Gly	Asp	Gly	Phe	Gly	Val	Ser	Lys	Leu	Glu	Val		
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Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu
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Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
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Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
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Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
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Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val
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Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
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Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe
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Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu
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Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg
165 170 175
Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
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Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp
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Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
210 215 220
Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
225 230 235 240

Leu Glu Phe Leu Asn Ser Val Met Ile Lys Phe Gly Asn Phe Val Pro
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 Cys Leu Tyr Pro Val Asp Leu Leu Glu Arg Leu Leu Ile Val Asp Asn
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 Ile Val Arg Leu Gly Ile Tyr Arg His Phe Glu Lys Glu Ile Lys Glu
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 Gly Arg Leu Asn Pro Ile Ala Asp Leu Glu Thr Thr Ala Leu Gly Phe
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 Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp
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 Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln
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 Pro Tyr Val Asn Asn Glu Lys Phe Leu Glu Leu Gly Lys Leu Asp Phe
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Pro	Ala	Val	Lys	Glu	Leu	Thr	Arg	Glu	Phe	Leu	Lys	Pro	Asp	Asp	Val																			
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Pro Ala Tyr Tyr Glu Leu Leu Gln Lys Leu Ile Glu Glu Ile Lys His
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Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile
50 55 60

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Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg
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cat ttt gaa cac gaa ata caa aca gct gct tta gat tac gtt tac aga 287
His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg
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Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser
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Lys Asp Leu Asn Ala Thr Ala Leu Gly Phe Arg Ala Leu Arg Leu His
115 120 125

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Arg Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn
130 135 140

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Gly Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys
145 150 155

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Gln Val Arg Ser Met Leu Ser Leu Leu Arg Ala Ser Glu Ile Ser Phe
160 165 170 175

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Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr
180 185 190

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195 200 205

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Ser Leu Leu Glu Arg Gly Glu Val Arg Ile Gly Val Ser Met Ala Cys
210 215 220

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Ser Val Pro Arg Trp Glu Ala Arg Ser Phe Leu Glu Ile Tyr Gly His
225 230 235

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Asn His Ser Trp Leu Lys Ser Asn Ile Asn Gln Lys Met Leu Lys Leu
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gcc aaa ttg gac ttc aat att ctg caa tgc aaa cat cac aag gag ata 815
Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile
260 265 270

cag ttt att aca agg tgg tgg aga gac tcg ggt ata tcg cag ctg aat 863

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Leu Leu Leu Thr Glu Met Glu Met Asp Asp Gly Asp His Asp Leu Ile	
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Lys Arg Leu Gln Ile Val Asp Thr Leu Glu Cys Leu Gly Ile Asp Arg	
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His Phe Glu His Glu Ile Gln Thr Ala Ala Leu Asp Tyr Val Tyr Arg	
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Trp Trp Asn Glu Lys Gly Ile Gly Glu Gly Ser Arg Asp Ser Phe Ser	
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Pro Gly Glu Lys Val Met Glu Glu Ala Lys Ala Phe Thr Arg Glu Tyr	
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Ala Lys Leu Asp Phe Asn Ile Leu Gln Cys Lys His His Lys Glu Ile	
260 265 270	
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Phe	Tyr	Arg	Lys	Arg	His	Val	Glu	Tyr	Tyr	Ser	Trp	Val	Val	Met	Cys	
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Ile	Phe	Glu	Pro	Glu	Phe	Ser	Glu	Ser	Arg	Ile	Ala	Phe	Ala	Lys	Thr	
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Ala	Ile	Leu	Cys	Thr	Val	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Ala	Thr	
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Ser	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Tyr	Ile	Lys	Ile	Ala	Phe	Gln	Phe	
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Phe	Phe	Asn	Thr	Val	Asn	Glu	Leu	Ile	Val	Glu	Ile	Val	Lys	Arg	Gln	
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Gly	Arg	Asp	Met	Thr	Thr	Ile	Val	Lys	Asp	Cys	Trp	Lys	Arg	Tyr	Ile	
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Glu	Ser	Tyr	Leu	Gln	Glu	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Ile	Pro	
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Thr	Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys	
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Ile	Val	Asn	Leu	Asn	Pro	Leu	Leu	Leu	Leu	Gly	Lys	Leu	Leu	Pro	Asp	
			435					440					445			
aac	att	ctg	gag	caa	ata	cat	tct	cca	tcc	aag	atc	ctg	gac	ctc	tta	1391
Asn	Ile	Leu	Glu	Gln	Ile	His	Ser	Pro	Ser	Lys	Ile	Leu	Asp	Leu	Leu	
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gaa	ttg	acg	ggc	aga	atc	gcc	gat	gac	tta	aaa	gat	ttc	gag	gac	gag	1439
Glu	Leu	Thr	Gly	Arg	Ile	Ala	Asp	Asp	Leu	Lys	Asp	Phe	Glu	Asp	Glu	
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Lys	Glu	Arg	Gly	Glu	Met	Ala	Ser	Ser	Leu	Gln</						

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Leu	Leu	Glu	Arg	Gly	Glu	Val	Arg	Ile	Gly	Val	Ser	Met	Ala	Cys	Ser	
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Val	Pro	Arg	Trp	Glu	Ala	Arg	Ser	Phe	Leu	Glu	Ile	Tyr	Gly	His	Asn	
				225					230					235		
His	Ser	Trp	Leu	Lys	Ser	Asn	Ile	Asn	Gln	Lys	Met	Leu	Lys	Leu	Ala	
				245					250					255		
Lys	Leu	Asp	Phe	Asn	Ile	Leu	Gln	Cys	Lys	His	His	Lys	Glu	Ile	Gln	
				260					265					270		
Phe	Ile	Thr	Arg	Trp	Trp	Arg	Asp	Ser	Gly	Ile	Ser	Gln	Leu	Asn	Phe	
				275					280					285		
Tyr	Arg	Lys	Arg	His	Val	Glu	Tyr	Tyr	Ser	Trp	Val	Val	Met	Cys	Ile	
				290					295					300		
Phe	Glu	Pro	Glu	Phe	Ser	Glu	Ser	Arg	Ile	Ala	Phe	Ala	Lys	Thr	Ala	
				305					310					315		
Ile	Leu	Cys	Thr	Val	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Ala	Thr	Leu	
				325					330					335		
His	Glu	Ile	Lys	Ile	Met	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Leu	Ser	
				340					345					350		
Leu	Thr	Asp	Asp	Leu	Pro	Asp	Tyr	Ile	Lys	Ile	Ala	Phe	Gln	Phe	Phe	
				355					360					365		
Phe	Asn	Thr	Val	Asn	Glu	Leu	Ile	Val	Glu	Ile	Val	Lys	Arg	Gln	Gly	
				370					375					380		
Arg	Asp	Met	Thr	Thr	Ile	Val	Lys	Asp	Cys	Trp	Lys	Arg	Tyr	Ile	Glu	
				385					390					395		
Ser	Tyr	Leu	Gln	Glu	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Ile	Pro	Thr	
				405					410					415		
Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys	Ile	
				420					425					430		
Val	Asn	Leu	Asn	Pro	Leu	Leu	Leu	Leu	Gly	Lys	Leu	Leu	Pro	Asp	Asn	
				435					440					445		
Ile	Leu	Glu	Gln	Ile	His	Ser	Pro	Ser	Lys	Ile	Leu	Asp	Leu	Leu	Glu	
				450					455					460		
Leu	Thr	Gly	Arg	Ile	Ala	Asp	Asp	Leu	Lys	Asp	Phe	Glu	Asp	Glu	Lys	
				465					470					475		

Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met Glu
565 570 575

[illegible]

aaa tgt tac gtc gaa ttt tac ttt tgg atg gct gca gcc atc tcc gag 383

Lys	Cys	Tyr	Val	Glu	Phe	Tyr	Phe	Trp	Met	Ala	Ala	Ala	Ile	Ser	Glu		
			115					120					125				
ccg	gag	ttt	tct	gga	agc	aga	gtt	gcc	ttc	aca	aaa	att	gct	ata	ctg	431	
Pro	Glu	Phe	Ser	Gly	Ser	Arg	Val	Ala	Phe	Thr	Lys	Ile	Ala	Ile	Leu		
		130					135					140					
atg	aca	atg	cta	gat	gac	ctg	tac	gat	act	cac	gga	acc	ttg	gac	caa	479	
Met	Thr	Met	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Gly	Thr	Leu	Asp	Gln		
		145					150				155						
ctc	aaa	atc	ttt	aca	gag	gga	gtg	aga	cga	tggt	gat	gtt	tcg	ttg	gta	527	
Leu	Lys	Ile	Phe	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Val	Ser	Leu	Val		
160					165				170						175		
gag	ggc	ctc	cca	gac	ttc	atg	aaa	att	gca	ttc	gag	ttc	tggt	tta	aag	575	
Glu	Gly	Leu	Pro	Asp	Phe	Met	Lys	Ile	Ala	Phe	Glu	Phe	Trp	Leu	Lys		
				180					185						190		
aca	tct	aat	gaa	ttg	att	gct	gaa	gct	gtt	aaa	gcg	caa	ggg	caa	gat	623	
Thr	Ser	Asn	Glu	Leu	Ile	Ala	Glu	Ala	Val	Lys	Ala	Gln	Gly	Gln	Asp		
			195					200					205				
atg	gcg	gcc	tac	ata	aga	aaa	aat	gca	tggt	gag	cga	tac	ctt	gaa	gct	671	
Met	Ala	Ala	Tyr	Ile	Arg	Lys	Asn	Ala	Trp	Glu	Arg	Tyr	Leu	Glu	Ala		
		210					215					220					
tat	ctg	caa	gat	gcg	gaa	tggt	ata	gcc	act	gga	cat	gtc	ccc	acc	ttt	719	
Tyr	Leu	Gln	Asp	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Val	Pro	Thr	Phe		
		225				230					235						
gat	gag	tac	ttg	aat	aat	ggc	aca	cca	aac	act	ggg	atg	tgt	gta	ttg	767	
Asp	Glu	Tyr	Leu	Asn	Asn	Gly	Thr	Pro	Asn	Thr	Gly	Met	Cys	Val	Leu		
					245					250					255		
aat	ttg	att	ccg	ctt	ctg	tta	atg	ggt	gaa	cat	tta	cca	atc	gac	att	815	
Asn	Leu	Ile	Pro	Leu	Leu	Leu	Met	Gly	Glu	His	Leu	Pro	Ile	Asp	Ile		
				260					265					270			
ctg	gag	caa	ata	ttc	ttg	ccc	tcc	agg	ttc	cac	cat	ctc	att	gaa	ttg	863	
Leu	Glu	Gln	Ile	Phe	Leu	Pro	Ser	Arg	Phe	His	His	Leu	Ile	Glu	Leu		
			275					280					285				
gct	tcc	agg	ctc	gtc	gat	gac	gcg	aga	gat	ttc	cag	gcg	gag	aag	gat	911	
Ala	Ser	Arg	Leu	Val	Asp	Asp	Ala	Arg	Asp	Phe	Gln	Ala	Glu	Lys	Asp		
		290					295					300					
cat	ggg	gat	tta	tcg	tgt	att	gag	tgt	tat	tta	aaa	gat	cat	cct	gag	959	
His	Gly	Asp	Leu	Ser	Cys	Ile	Glu	Cys	Tyr	Leu	Lys	Asp	His	Pro	Glu		
		305				310					315						
tct	aca	gta	gaa	gat	gct	tta	aat	cat	gtt	aat	ggc	ctc	ctt	ggc	aat	1007	
Ser	Thr	Val	Glu	Asp	Ala	Leu	Asn	His	Val	Asn	Gly	Leu	Leu	Gly	Asn		
					325					330					335		
tgc	ctt	ctg	gaa	atg	aat	tggt	aag	ttc	tta	aag	aag	cag	gac	agt	gtg	1055	
Cys	Leu	Leu	Glu	Met	Asn	Trp	Lys	Phe	Leu	Lys	Lys	Gln	Asp	Ser	Val		
				340					345					350			
cca	ctc	tcg	tgt	aag	aag	tac	agc	ttc	cat	gta	ttg	gca	cga	agc	atc	1103	
Pro	Leu	Ser	Cys	Lys	Lys	Tyr	Ser	Phe	His	Val	Leu	Ala	Arg	Ser	Ile		

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360

365

caa ttc atg tac aat caa ggc gat ggc ttc tcc att tcg aac aaa gtg 1151
Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val
370 375 380

atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg cct att tga 1199
Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

tagtagatac tagatagtag attagtagct attagtattt atttcatatc aatatttact 1259
aatgctgatg atggtaaag tccattcaga ccaatctttg gtttattgga cttaaataaa 1319
tgaattaatt agtttgtttt aaaattgtac tattttactgt tggaaataat gttttcatta 1379
ttgaaataac tagcacaact attttagtgt ggttgat 1416

<210> 20

<211> 398

<212> PRT

<213> Abies grandis

<400> 20

Lys Val Met Glu Glu Ala Lys Ala Phe Thr Thr Asn Tyr Leu Lys Lys
1 5 10 15

Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu Gly
20 25 30

Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln Arg
35 40 45

Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu
50 55 60

Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp
65 70 75 80

Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser
85 90 95

Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys
100 105 110

Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro
115 120 125

Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met
130 135 140

Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu
145 150 155 160

Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu
165 170 175

Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr
180 185 190

1151
1199
1259
1319
1379
1416

Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn
245 250 255

Leu Ile Pro Leu Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln
355 360 365

Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
385 390 395

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide PCR primer E wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer E wherein the letter n represents
inosine

<400> 21
ggngaramrr tnatggarga rgc

<210> 22

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
oligonucleotide primer F wherein the letter "n"
represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer F wherein the letter n represents
inosine

<400> 22
garytnrcary tnhbnmgntg gtgg

24

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer G wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(21)
<223> PCR primer G wherein the letter n represents
inosine

<400> 23
ccarttnarn ccytnacrt c

21

<210> 24
<211> 533
<212> DNA
<213> Abies grandis

<400> 24
ggggaaaaaa tgatggagga agctgaaatc ttctctacca aatattttaaa agaagccctg 60
caaaaagattc cggctctccag tcttttcgca gagatcgggg acgtttttgga atatggttgg 120
cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtcttttg acaggacact 180
gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240
aacatctttc aatccttact cgcatatccg cattgcaacc cattctgaca atggacatcc 300
cctttcctga tcatatcctc aaggaagttg acttcccatc aaagcttaac gacttggcat 360
gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420
aagaagcttc ctctatatca tgttatatga aagacaatcc tggagtatca gaggaagatg 480

ctctcgatca tatcaacgcc atgatcagtg acgaagtcaa aggcttcaat tgg

533

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif on which the sequence of Primer D
was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa
at
position number 4 represents Ile or Tyr or Phe, Xaa at position number 6
represents Ala or Val and Xaa at position number 8 represents Ala or Gly

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid motif on which sequence of
primer D was based

<400> 25
Asp Asp Xaa Xaa Asp Xaa Tyr Xaa
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif on which the sequence of Primer E
was based wherein Xaa at position 3 represents Lys or Thr, Xaa at
position
4 represents Val or Ile, Xaa at position 6 represents Glu or Asp

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid sequence on which the
sequence of primer E was based

<400> 26
Gly Glu Xaa Xaa Met Xaa Glu Ala
1 5

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid sequence on which the sequence of
primer F was based wherein Xaa at position 2 represents Phe or Tyr or
Asp

Xaa at position 3 represents Ile or Leu, Xaa at position 4 represents Thr or Leu
or Arg

<220>
<221> SITE
<222> (1)..(7)
<223> conserved amino acid sequence on which the
sequence of primer F was based

<400> 27
Gln Xaa Xaa Xaa Arg Trp Trp
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif on which the sequence of primer G
was based wherein Xaa at position 6 represents Phe or Leu

<220>
<221> SITE
<222> (1)..(8)
<223> conserved amino acid sequence on which the
sequence of primer G was based

<400> 28
Asp Val Ile Lys Gly Xaa Asn Trp
1 5

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T3 primer
oligonucleotide sequence

<400> 29
aattaaccct cactaaagg

20

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: T7
oligonucleotide primer sequence

<400> 30
gtaatacgac tcactatagg gc

22

Sequence

<210> 31
<211> 2205
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (57)..(1943)
<223> Clone AG3.48

<400> 31
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Met
1
gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc ctg cgc aag 107
Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys
5 10 15
tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155
Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile
20 25 30
cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203
Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser Met
35 40 45
agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251
Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg
50 55 60 65
ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299
Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser
70 75 80
cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347
Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg
85 90 95
tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395
Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp
100 105 110
gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443
Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile
115 120 125
gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491
Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu
130 135 140 145
ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc 539
Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly
150 155 160
att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg 587
Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr Ala
165 170 175
ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag 635

[illegible]

[illegible]

<400>	32															
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Lys	Ser	Leu	Ile	Ser	Ser	Ile	His	Glu	His	Lys	Pro	Pro	Tyr	Arg	Thr	
			20					25					30			
Ile	Pro	Asn	Leu	Gly	Met	Arg	Arg	Arg	Gly	Lys	Ser	Val	Thr	Pro	Ser	
		35					40					45				
Met	Ser	Ile	Ser	Leu	Ala	Thr	Ala	Ala	Pro	Asp	Asp	Gly	Val	Gln	Arg	
	50					55					60					
Arg	Ile	Gly	Asp	Tyr	His	Ser	Asn	Ile	Trp	Asp	Asp	Asp	Phe	Ile	Gln	
65					70					75					80	
Ser	Leu	Ser	Thr	His	Tyr	Gly	Glu	Pro	Ser	Tyr	Gln	Glu	Arg	Ala	Glu	
				85				90						95		
Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	Leu	Asp	
			100					105					110			
Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	Leu	Trp	
		115					120					125				
Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	Lys	Asn	
	130					135					140					
Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	Glu	Asn	
145					150					155					160	
Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	Ser	Thr	
			165						170					175		
Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	Ser	Pro	
			180					185					190			
Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser	
		195					200					205				
Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg	
	210				215						220					
Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu	
225				230					235						240	
Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val	
				245					250					255		
Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His	
			260					265					270			
Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu	
	275					280						285				

Lys 290	Thr	Ser	Ala	Trp	Leu 295	Asn	Lys	Asn	Ala	Gly 300	Lys	Lys	Leu	Leu	
Glu 305	Leu	Ala	Lys	Leu	Glu 310	Phe	Asn	Ile	Phe	Asn 315	Ser	Leu	Gln	Gln	Lys 320
Glu	Leu	Gln	Tyr	Leu 325	Leu	Arg	Trp	Trp	Lys 330	Glu	Ser	Asp	Leu	Pro 335	Lys
Leu	Thr	Phe	Ala 340	Arg	His	Arg	His	Val 345	Glu	Phe	Tyr	Thr	Leu 350	Ala	Ser
Cys	Ile	Ala 355	Ile	Asp	Pro	Lys	His 360	Ser	Ala	Phe	Arg	Leu 365	Gly	Phe	Ala
Lys 370	Met	Cys	His	Leu	Val	Thr 375	Val	Leu	Asp	Asp	Ile 380	Tyr	Asp	Thr	Phe
Gly 385	Thr	Ile	Asp	Glu	Leu 390	Glu	Leu	Phe	Thr	Ser 395	Ala	Ile	Lys	Arg	Trp 400
Asn	Ser	Ser	Glu	Ile 405	Glu	His	Leu	Pro	Glu 410	Tyr	Met	Lys	Cys	Val 415	Tyr
Met	Val	Val	Phe 420	Glu	Thr	Val	Asn	Glu 425	Leu	Thr	Arg	Glu	Ala 430	Glu	Lys
Thr	Gln	Gly 435	Arg	Asn	Thr	Leu	Asn 440	Tyr	Val	Arg	Lys	Ala 445	Trp	Glu	Ala
Tyr	Phe 450	Asp	Ser	Tyr	Met	Glu 455	Glu	Ala	Lys	Trp	Ile 460	Ser	Asn	Gly	Tyr
Leu 465	Pro	Thr	Phe	Glu	Glu 470	Tyr	His	Glu	Asn 475	Gly	Lys	Val	Ser	Ser	Ala 480
Tyr	Arg	Val	Ala	Thr 485	Leu	Gln	Pro	Ile	Leu 490	Thr	Leu	Asn	Ala	Trp 495	Leu
Pro	Asp	Tyr	Ile 500	Leu	Lys	Gly	Ile	Asp 505	Phe	Pro	Ser	Arg	Phe 510	Asn	Asp
Leu	Ala	Ser 515	Ser	Phe	Leu	Arg	Leu 520	Arg	Gly	Asp	Thr	Arg 525	Cys	Tyr	Lys
Ala 530	Asp	Arg	Asp	Arg	Gly	Glu 535	Glu	Ala	Ser	Cys	Ile 540	Ser	Cys	Tyr	Met
Lys 545	Asp	Asn	Pro	Gly	Ser 550	Thr	Glu	Glu	Asp	Ala 555	Leu	Asn	His	Ile	Asn 560
Ala	Met	Val	Asn	Asp 565	Ile	Ile	Lys	Glu	Leu 570	Asn	Trp	Glu	Leu	Leu 575	Arg
Ser	Asn	Asp	Asn 580	Ile	Pro	Met	Leu	Ala 585	Lys	Lys	His	Ala	Phe 590	Asp	Ile
Thr	Arg	Ala 595	Leu	His	His	Leu	Tyr 600	Ile	Tyr	Arg	Asp	Gly 605	Phe	Ser	Val
Ala	Asn	Lys	Glu	Thr	Lys	Lys	Leu	Val	Met	Glu	Thr	Leu	Leu	Glu	Ser

610

615

620

Met Leu Phe
625

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 BamHI

<400> 33
caaagggatc cagaatggct ctgg 24

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 Not I

<400> 34
agtaagcggc cgctttttaa tcataccac 30

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 EcoRI

<400> 35
ctgcaggaat tcggcacgag c 21

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 SmaI

<400> 36
catagccccg ggcatagatt tgagctg 27

<210> 37
<211> 30
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 NdeI

<400> 37

ggcaggaaca tatggctctc ctttctatcg

30

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 10 BamHI

<400> 38

tctagaacta gtggatcccc cgggctgcag

30

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer JB29

<400> 39

ctaccattcc aatatctg

18

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2-8

<400> 40

gttggatctt agaagttccc

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-9

<400> 41

tttccattcc aacctctggg

20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-11

<400> 42
cgtaatggaa agctctggcg 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 7-1

<400> 43
ccttacacgc ctttggatgg 20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide sequence 7-3

<400> 44
tctgttgatc caggatggtc 20

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif common to all prenyl transferases wherein Xaa at
position
3 and 4 represents any amino acid

<400> 45
Asp Asp Xaa Xaa Asp
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide primers can be synthesized that hybridize to the monoterpene synthases of the present invention, wherein Xaa at position 4 represents
Leu or Ile or Val

<400> 46

His Ser Asn Xaa Trp Asp Asp Asp
1 5

<210> 47

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotides can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 47

Ala Leu Asp Tyr Val Tyr
1 5

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 48

Glu Leu Ala Lys Leu Glu Phe
1 5

<210> 49

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention

<400> 49

Arg Trp Trp Lys Glu Ser
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100

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to monoterpene synthase
clones of the present invention, wherein Xaa at position 1 represents
Val
or Ile or Leu

<400> 50
Xaa Leu Asp Asp Met Tyr Asp
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to monoterpene synthase
clones of the present invention wherein Xaa at position 1 represents
Val
or Ile or Leu

<400> 51
Xaa Leu Asp Asp Leu Tyr Asp
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to the monoterpene
synthase clones of the present invention, wherein Xaa at position 1
represents Val or Ile or Leu

<400> 52
Xaa Leu Asp Asp Ile Tyr Asp
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpene synthase clones of the present invention, wherein Xaa at position 6 represents Asn or His

<400> 53
Cys Tyr Met Lys Asp Xaa Pro
1 5

<210> 54
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet

<400> 54
atgatgatg 9

<210> 55
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide sequence that corresponds to peptide sequence MetMetMet

<400> 55
tactactac 9

<210> 56
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet, n is inosine

<400> 56
nacnacnac 9

<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide corresponding to amino acid sequence set forth in SEQ ID NO:46

<220>
<221> misc_feature
<222> (1)..(24)
<223> Oligonucleotide that corresponds to the conserved
amino acid sequence set forth in SEQ ID NO:46

<400> 57
gtgtcggttg agaccctgct gctg

24

<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:47

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:47

<400> 58
cgggagctga tgcagatg

18

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:48

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:48

<400> 59
ctcgagcggg tgcagctcaa g

21

<210> 60
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:49

<220>
 <221> misc_feature
 <222> (1)..(18)
 <223> Oligonucleotide that corresponds to conserved
 amino acid sequence set forth in SEQ ID NO:49

<400> 60
 gccaccacct tcctctcg

18

<210> 61
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide sequence corresponding to amino
 acid sequence set forth in SEQ ID NO:50

<220>
 <221> misc_feature
 <222> (1)..(21)
 <223> Oligonucleotide sequence corresponding to amino
 acid sequence set forth in SEQ ID NO:50

<400> 61
 gaggagctgc tgtacatgct g

21

<210> 62
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide corresponding to amino acid
 sequence set forth in SEQ ID NO:51

<220>
 <221> misc_feature
 <222> (1)..(21)
 <223> Oligonucleotide corresponding to conserved amino
 acid sequence set forth in SEQ ID NO:51

<400> 62
 gaggagctgc tggagatgct g

21

<210> 63
 <211> 293
 <212> DNA
 <213> Abies grandis

<400> 63
 cttaatgaat tggcgcaaga ggctgagaag actcaaggca gagatacgt caactatatt 60
 cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

gaa aaa ggc att gga tgt ggg agg gag agt gtt gtg act gac ctc aac 533
Glu Lys Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn
155 160 165

Species	Abundance	Species	Abundance	Species	Abundance
^{12}C	100	^{16}O	100	^{28}Si	100
^{13}C	1.1	^{17}O	0.04	^{29}Si	4.7
^{14}C	0.01	^{18}O	0.2	^{30}Si	3.1
^{15}N	0.004	^{19}F	100	^{31}P	100
^{16}O	100	^{20}Ne	9.2	^{32}S	95.0
^{17}O	0.04	^{21}Ne	0.27	^{33}S	0.75
^{18}O	0.2	^{22}Ne	9.0	^{34}S	4.2
^{19}F	100	^{23}Ne	0.0027	^{36}S	0.02
^{20}Ne	9.2	^{24}Mg	78.9	^{37}Cl	24.2
^{21}Ne	0.27	^{25}Mg	12.0	^{35}Cl	75.8
^{22}Ne	9.0	^{26}Mg	11.0	^{36}S	0.02
^{23}Ne	0.0027	^{27}Al	100	^{38}S	0.0005
^{24}Mg	78.9	^{28}Si	100	^{39}Ar	0.0001
^{25}Mg	12.0	^{29}Si	4.7	^{40}Ar	99.6
^{26}Mg	11.0	^{30}Si	3.1	^{41}K	6.7
^{27}Al	100	^{31}P	100	^{42}Ca	98.9
^{28}Si	100	^{32}S	95.0	^{43}Ca	0.14
^{29}Si	4.7	^{33}S	0.75	^{44}Ca	2.2
^{30}Si	3.1	^{34}S	4.2	^{46}Ca	0.004
^{31}P	100	^{36}S	0.02	^{48}Ca	0.006
^{32}S	95.0	^{38}S	0.0005	^{50}Ca	0.0001
^{33}S	0.75	^{40}Ar	99.6	^{52}Cr	71.7
^{34}S	4.2	^{41}K	6.7	^{53}Cr	2.8
^{36}S	0.02	^{42}Ca	98.9	^{54}Cr	8.3
^{37}Cl	24.2	^{43}Ca	0.14	^{56}Fe	91.7
^{35}Cl	75.8	^{44}Ca	2.2	^{57}Fe	0.022
^{36}S	0.02	^{46}Ca	0.004	^{58}Fe	0.0002
^{38}S	0.0005	^{48}Ca	0.006	^{59}Co	100
^{39}Ar	0.0001	^{50}Ca	0.0001	^{60}Co	0.0001
^{40}Ar	99.6	^{52}Cr	71.7	^{61}Ni	0.0001
^{41}K	6.7	^{53}Cr	2.8	^{62}Ni	0.0001
^{42}Ca	98.9	^{54}Cr	8.3	^{64}Ni	0.0001
^{43}Ca	0.14	^{56}Fe	91.7	^{66}Ni	0.0001
^{44}Ca	2.2	^{57}Fe	0.022	^{68}Ni	0.0001
^{46}Ca	0.004	^{58}Fe	0.0002	^{70}Ni	0.0001
^{48}Ca	0.006	^{59}Co	100	^{72}Ni	0.0001
^{50}Ca	0.0001	^{60}Co	0.0001	^{74}Ni	0.0001
^{52}Cr	71.7	^{61}Ni	0.0001	^{76}Ni	0.0001
^{53}Cr	2.8	^{62}Ni	0.0001	^{78}Ni	0.0001
^{54}Cr	8.3	^{64}Ni	0.0001	^{80}Ni	0.0001
^{56}Fe	91.7	^{66}Ni	0.0001	^{82}Ni	0.0001
^{57}Fe	0.022	^{68}Ni	0.0001	^{84}Ni	0.0001
^{58}Fe	0.0002	^{70}Ni	0.0001	^{86}Ni	0.0001
^{59}Co	100	^{72}Ni	0.0001	^{88}Ni	0.0001
^{60}Co	0.0001	^{74}Ni	0.0001	^{90}Ni	0.0001
^{61}Ni					

Tyr Met Met Val Tyr His Thr Val Asn Glu Met Ala Arg Val Ala Glu	
410 415 420	
aag gct caa ggc cga gac acg ctc aac tat gca aga cag gct tgg gag	1349
Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Gln Ala Trp Glu	
425 430 435	
gcg tgt ttt gat tcg tat atg cag gaa gca aag tgg atc gcc act ggt	1397
Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala Lys Trp Ile Ala Thr Gly	
440 445 450	
tat ctg ccc acg ttt gag gag tac ttg gag aac ggg aaa gtt agc tct	1445
Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Gly Lys Val Ser Ser	
455 460 465 470	
gct cat cgc cca tgc gca ctg caa ccc att ctg acg ttg gac atc ccc	1493
Ala His Arg Pro Cys Ala Leu Gln Pro Ile Leu Thr Leu Asp Ile Pro	
475 480 485	
ttt cct gat cac atc ctc aag gaa gtt gac ttc cca tcg aag ctc aat	1541
Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn	
490 495 500	
gac ttg ata tgt atc atc ctt cga tta aga ggt gat aca cgg tgc tac	1589
Asp Leu Ile Cys Ile Ile Leu Arg Glu Asp Thr Arg Cys Tyr	
505 510 515	
aag gca gac agg gcc cgt gga gaa gaa gct tcg tct ata tca tgt tat	1637
Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr	
520 525 530	
atg aaa gac aat cct gga tta acg gaa gaa gat gct ctg aat cat atc	1685
Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile	
535 540 545 550	
aac ttc atg atc agg gac gca atc aga gaa tta aat tgg gag ctt cta	1733
Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu	
555 560 565	
aag cca gac aac agt gtt ccc atc act tcc aag aaa cac gca ttt gac	1781
Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp	
570 575 580	
ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc	1829
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser	
585 590 595	
ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa	1877
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu	
600 605 610	
cct gtg cct ttg taacaacact tcaaactctac aatattaact gaggatgcc	1929
Pro Val Pro Leu	
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tatgggtgta tatagggcac acaaaaataa atatggttgt gttagtaaag ctgtaattta	1989
tgaaaaaaaa aaaaaaaaaa aaaa	2013

<211> 618
<212> PRT
<213> Abies grandis

<400> 65

Met	Ala	Leu	Leu	Ser	Ile	Thr	Pro	Leu	Val	Ser	Arg	Ser	Cys	Leu	Ser	1	5	10	15
Ser	Ser	His	Glu	Ile	Lys	Ala	Leu	Arg	Arg	Thr	Ile	Pro	Thr	Leu	Gly	20	25	30	
Ile	Cys	Arg	Pro	Gly	Lys	Ser	Val	Ala	His	Ser	Ile	Asn	Met	Cys	Leu	35	40	45	
Thr	Ser	Val	Ala	Ser	Thr	Asp	Ser	Val	Gln	Arg	Arg	Val	Gly	Asn	Tyr	50	55	60	
His	Ser	Asn	Leu	Trp	Asp	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ile	Ser	Thr	65	70	75	80
Pro	Tyr	Gly	Ala	Pro	Asp	Tyr	Arg	Glu	Arg	Ala	Asp	Arg	Leu	Ile	Gly	85	90	95	
Glu	Val	Lys	Asp	Ile	Met	Phe	Asn	Phe	Lys	Ser	Leu	Glu	Asp	Gly	Gly	100	105	110	
Asn	Asp	Leu	Leu	Gln	Arg	Leu	Leu	Leu	Val	Asp	Asp	Val	Glu	Arg	Leu	115	120	125	
Gly	Ile	Asp	Arg	His	Phe	Lys	Lys	Glu	Ile	Lys	Thr	Ala	Leu	Asp	Tyr	130	135	140	
Val	Asn	Ser	Tyr	Trp	Asn	Glu	Lys	Gly	Ile	Gly	Cys	Gly	Arg	Glu	Ser	145	150	155	160
Val	Val	Thr	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Gly	Leu	Arg	Thr	Leu	Arg	165	170	175	
Leu	His	Gly	Tyr	Thr	Val	Ser	Ser	Asp	Val	Leu	Asn	Val	Phe	Lys	Asp	180	185	190	
Lys	Asn	Gly	Gln	Phe	Ser	Ser	Thr	Ala	Asn	Ile	Gln	Ile	Glu	Gly	Glu	195	200	205	
Ile	Arg	Gly	Val	Leu	Asn	Leu	Phe	Arg	Ala	Ser	Leu	Val	Ala	Phe	Pro	210	215	220	
Gly	Glu	Lys	Val	Met	Asp	Glu	Ala	Glu	Thr	Phe	Ser	Thr	Lys	Tyr	Leu	225	230	235	240
Arg	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Ala	Ser	Ser	Ile	Leu	Ser	Leu	Glu	245	250	255	
Ile	Arg	Asp	Val	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	260	265	270	
Glu	Ala	Arg	Asn	Tyr	Met	Asp	Val	Phe	Gly	Gln	His	Thr	Lys	Asn	Lys	275	280	285	
Asn	Ala	Ala	Glu	Lys	Leu	Leu	Glu	Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	290	295	300	

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1				5					10					15	
Leu	Lys	Ser	Leu	Ile	Ser	Ser	Ser	Asn	Val	Gln	Lys	Ala	Leu	Cys	Ile
			20					25					30		
Ser	Thr	Ala	Val	Pro	Thr	Leu	Arg	Met	Arg	Arg	Arg	Gln	Lys	Ala	Leu
		35					40					45			
Val	Ile	Asn	Met	Lys	Leu	Thr	Thr	Val	Ser	His	Arg	Asp	Asp	Asn	Gly
	50					55					60				
Gly	Gly	Val	Leu	Gln	Arg	Arg	Ile	Ala	Asp	His	His	Pro	Asn	Leu	Trp
65					70				75					80	
Glu	Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ser	Ser	Pro	Tyr	Gly	Gly	Ser	Ser
			85						90					95	
Tyr	Ser	Glu	Arg	Ala	Val	Thr	Val	Val	Glu	Glu	Val	Lys	Glu	Met	Phe
			100					105					110		
Asn	Ser	Ile	Pro	Asn	Asn	Arg	Glu	Leu	Phe	Gly	Ser	Gln	Asn	Asp	Leu
		115					120					125			
Leu	Thr	Arg	Leu	Trp	Met	Val	Asp	Ser	Ile	Glu	Arg	Leu	Gly	Ile	Asp
	130					135					140				
Arg	His	Phe	Gln	Asn	Glu	Ile	Arg	Val	Ala	Leu	Asp	Tyr	Val	Tyr	Ser
145				150						155				160	
Tyr	Trp	Lys	Glu	Lys	Glu	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Thr	Phe
			165						170					175	
Pro	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Arg	Thr	Leu	Arg	Leu	His
			180					185					190		
Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Glu	Tyr	Phe	Lys	Asp	Gln	Lys
		195					200					205			
Gly	His	Phe	Ala	Cys	Pro	Ala	Ile	Leu	Thr	Glu	Gly	Gln	Ile	Thr	Arg
	210					215					220				
Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Leu	Val	Ala	Phe	Pro	Gly	Glu

225	230										235					240				
Lys	Val	Met	Glu	Glu	Ala	Glu	Ile	Phe	Ser	Ala	Ser	Tyr	Leu	Lys	Glu					
				245					250					255						
Val	Leu	Gln	Lys	Ile	Pro	Val	Ser	Ser	Phe	Ser	Arg	Glu	Ile	Glu	Tyr					
			260					265					270							
Val	Leu	Glu	Tyr	Gly	Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg					
		275					280					285								
Asn	Tyr	Ile	Asp	Val	Tyr	Gly	Gln	Asp	Ser	Tyr	Glu	Ser	Ser	Asn	Glu					
	290					295					300									
Met	Pro	Tyr	Val	Asn	Thr	Gln	Lys	Leu	Leu	Lys	Leu	Ala	Lys	Leu	Glu					
305					310					315					320					
Phe	Asn	Ile	Phe	His	Ser	Leu	Gln	Gln	Lys	Glu	Leu	Gln	Tyr	Ile	Ser					
				325					330					335						
Arg	Trp	Trp	Lys	Asp	Ser	Cys	Ser	Ser	His	Leu	Thr	Phe	Thr	Arg	His					
			340					345					350							
Arg	His	Val	Glu	Tyr	Tyr	Thr	Met	Ala	Ser	Cys	Ile	Ser	Met	Glu	Pro					
		355					360					365								
Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	Phe	Val	Lys	Thr	Cys	His	Leu	Leu					
	370					375					380									
Thr	Val	Leu	Asp	Asp	Met	Tyr	Asp	Thr	Phe	Gly	Thr	Leu	Asp	Glu	Leu					
385					390					395					400					
Gln	Leu	Phe	Thr	Thr	Ala	Phe	Lys	Arg	Trp	Asp	Leu	Ser	Glu	Thr	Lys					
				405					410					415						
Cys	Leu	Pro	Glu	Tyr	Met	Lys	Ala	Val	Tyr	Met	Asp	Leu	Tyr	Gln	Cys					
			420					425					430							
Leu	Asn	Glu	Leu	Ala	Gln	Glu	Ala	Glu	Lys	Thr	Gln	Gly	Arg	Asp	Thr					
		435					440					445								
Leu	Asn	Tyr	Ile	Arg	Asn	Ala	Tyr	Glu	Ser	His	Phe	Asp	Ser	Phe	Met					
	450					455					460									
His	Glu	Ala	Lys	Trp	Ile	Ser	Ser	Gly	Tyr	Leu	Pro	Thr	Phe	Glu	Glu					
465					470					475					480					
Tyr	Leu	Lys	Asn	Gly	Lys	Val	Ser	Ser	Gly	Ser	Arg	Thr	Ala	Thr	Leu					
				485					490					495						
Gln	Pro	Ile	Leu	Thr	Leu	Asp	Val	Pro	Leu	Pro	Asn	Tyr	Ile	Leu	Gln					
			500					505					510							
Glu	Ile	Asp	Tyr	Pro	Ser	Arg	Phe	Asn	Asp	Leu	Ala	Ser	Ser	Leu	Leu					
		515					520					525								
Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly					
	530					535					540									
Glu	Glu	Ala	Ser	Ala	Ile	Ser	Cys	Tyr	Met	Lys	Asp	His	Pro	Gly	Ser					
545					550					555					560					

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu
625 630 635

<210> 70

<211> 696

<212> DNA

<213> Abies grandis

<400> 70

gcatttaaga gatgggatcc gtctgccaca gatttgcttc cagagtatat gaaaggggtg 60

tacatggtgg ttacgaaac cgtaaataaa attgctcgag aggcagacaa gtctcaaggc 120

cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatatgaaa 180

gaagctgagt ggatctccag tgggttatctg ccaacgtttg aggagtacat ggagaccagc 240

aaagttagtt ttggttatcg catattcgca ttgcaacca tcctcactat ggatgttccc 300

cttactcacc acatctcgca ggaaatagac ttccattga ggtttaatga cttaatatgt 360

tccatccttc gacttaaaaa tgacactcgc tgctacaagg cggacagggc ccgtggagaa 420

gaagcttcgt gtatatcgtg ttatatgaaa gagaatcctg gatcaacaga ggaagatgct 480

atcaatcata tcaacgctat ggtcaataac ttaatcaaag aagtgaattg ggagcttctc 540

cgacaggacg gcaccgctca tattgcttgc aagaaacacg cttttgacat cctcaaaggc 600

tcccttcacg gctacaaata ccgagatggg ttcagcgttg ccaacaagga aaccaagaat 660

tgggtgagga gaacagtcct tgagtcgttg cctttg 696

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> Reverse RACE primer 10-2

<400> 71
acgaagcttc ttctccacgg

20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> Reverse RACE primer 10-4

<400> 72
ggatcccatc tcttaactgc

20

Sequence

<210> 73
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(27)
<223> PCR primer AP1

<400> 73
ccatccta atc acgactcact atagggc

27

<210> 74
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer AP2

<400> 74
actcactata gggctcgagc ggc

23

<210> 75
<211> 24

<212> DNA
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<220>
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oligonucleotide

<220>
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<222> (1)..(24)
<223> PCR primer AG9F

<400> 75
atggctcttg tttctatctt gccc

24

<210> 76
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<212> DNA
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<220>
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oligonucleotide

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<222> (1)..(24)
<223> PCR primer AG9R

<400> 76
ttacaaaggc acagactcaa ggac

24

<210> 77
<211> 1890
<212> DNA
<213> Abies grandis

<220>
<221> CDS
<222> (1)..(1890)

<400> 77
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Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca 96
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc 144
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa 192
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata 240

305				310				315				320				
caa Gln	cag Gln	aga Arg	gag Glu	cta Leu 325	aaa Lys	gac Asp	ctc Leu	tcc Ser	aga Arg 330	tgg Trp	tgg Trp	aaa Lys	gat Asp	tcg Ser 335	ggt Gly	1008
ttc Phe	tct Ser	cac His	ctg Leu 340	aca Thr	ttt Phe	tct Ser	cgg Arg	cat His 345	cgt Arg	cat His	gtg Val	gaa Glu	ttc Phe 350	tac Tyr	gct Ala	1056
ctg Leu	gca Ala	tct Ser 355	tgc Cys	att Ile	gaa Glu	act Thr	gat Asp 360	cgc Arg	aaa Lys	cat His	tcc Ser	gga Gly 365	ttc Phe	aga Arg	ctc Leu	1104
ggc Gly	ttt Phe 370	gcc Ala	aaa Lys	atg Met	tgt Cys	cat His 375	ctt Leu	atc Ile	acg Thr	gtt Val	ttg Leu 380	gac Asp	gat Asp	ata Ile	tac Tyr	1152
gac Asp 385	acc Thr	ttt Phe	gga Gly	aca Thr	atg Met 390	gag Glu	gag Glu	ctg Leu	gaa Glu	ctc Leu 395	ttc Phe	act Thr	gca Ala	gca Ala	ttt Phe 400	1200
aag Lys	aga Arg	tgg Trp	gat Asp	ccg Pro 405	tct Ser	gcc Ala	aca Thr	gat Asp	ttg Leu 410	ctt Leu	cca Pro	gag Glu	tat Tyr	atg Met 415	aaa Lys	1248
ggg Gly	ttg Leu	tac Tyr	atg Met 420	gtg Val	gtt Val	tac Tyr	gaa Glu	acc Thr 425	gta Val	aat Asn	gaa Glu	att Ile	gct Ala 430	cga Arg	gag Glu	1296
gca Ala	gac Asp	aag Lys 435	tct Ser	caa Gln	ggc Gly	cga Arg	gag Glu 440	acg Thr	ctc Leu	aac Asn	gat Asp	gct Ala 445	cga Arg	cga Arg	gct Ala	1344
tgg Trp	gag Glu	gcc Ala	tat Tyr	ctt Leu	gat Asp	tcg Ser 455	tat Tyr	atg Met	aaa Lys	gaa Glu	gct Ala 460	gag Glu	tgg Trp	atc Ile	tcc Ser	1392
agt Ser 465	ggt Gly	tat Tyr	ctg Leu	cca Pro	acg Thr 470	ttt Phe	gag Glu	gag Glu	tac Tyr	atg Met 475	gag Glu	acc Thr	agc Ser	aaa Lys	gtt Val 480	1440
agt Ser	ttt Phe	ggt Gly	tat Tyr	cgc Arg 485	ata Ile	ttc Phe	gca Ala	ttg Leu	caa Gln 490	ccc Pro	atc Ile	ctc Leu	act Thr	atg Met 495	gat Asp	1488
gtt Val	ccc Pro	ctt Leu	act Thr 500	cac His	cac His	atc Ile	ctg Leu	cag Gln 505	gaa Glu	ata Ile	gac Asp	ttt Phe	cca Pro 510	ttg Leu	agg Arg	1536
ttt Phe	aat Asn 515	gac Asp	tta Leu	ata Ile	tgt Cys	tcc Ser	atc Ile 520	ctt Leu	cga Arg	ctt Leu	aaa Lys	aat Asn 525	gac Asp	act Thr	cgc Arg	1584
tgc Cys	tac Tyr 530	aag Lys	gcg Ala	gac Asp	agg Arg	gcc Ala 535	cgt Arg	gga Gly	gaa Glu	gaa Glu	gct Ala 540	tcg Ser	tgt Cys	ata Ile	tcg Ser	1632
tgt Cys 545	tat Tyr	atg Met	aaa Lys	gag Glu	aat Asn 550	cct Pro	gga Gly	tca Ser	aca Thr	gag Glu 555	gaa Glu	gat Asp	gct Ala	atc Ile	aat Asn 560	1680

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<210> 78
<211> 630
<212> PRT
<213> Abies grandis

<400> 78
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   1                               5                10              15

Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
      20                      25             30

Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
     35                     40            45

Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
    50                   55           60

Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
  65                        70          75

Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala
     85                    90          95

Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala
    100                  105         110

Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu
   115                 120        125

Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys
   130                 135       140

Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu
  145                     150        155

Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser
   165                 170       175
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Thr Ala Leu Gly Phe Arg Ile Leu Arg Leu His Gly Tyr Ser Val Ser
180 185 190

Ser Asp Val Leu Glu His Phe Lys Glu Glu Lys Glu Lys Gly Gln Phe
195 200 205

Val Cys Ser Ala Ile Gln Thr Glu Glu Glu Ile Lys Ser Val Leu Asn
210 215 220

Leu Phe Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu
225 230 235 240

Glu Ala Glu Ile Phe Ser Lys Ile Tyr Leu Lys Glu Ala Leu Gln Asn
245 250 255

Ile Ala Val Ser Ser Leu Ser Arg Glu Ile Glu Tyr Val Leu Glu Asp
260 265 270

Gly Trp Gln Thr Asn Met Pro Arg Leu Glu Thr Arg Asn Tyr Ile Asp
275 280 285

Val Leu Gly Glu Asn Asp Arg Asp Glu Thr Leu Tyr Met Asn Met Glu
290 295 300

Lys Leu Leu Glu Ile Ala Lys Leu Glu Phe Asn Ile Phe His Ser Leu
305 310 315 320

Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly
325 330 335

Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala
340 345 350

Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu
355 360 365

Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr
370 375 380

Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe
385 390 395 400

Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys
405 410 415

Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu
420 425 430

Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala
435 440 445

Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser
450 455 460

Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val
465 470 475 480

Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp
485 490 495

Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg

[illegible]

30

30

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<210> 81
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
      oligonucleotide
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```
<220>  
<221> misc_feature  
<222> (1)..(30)  
<223> Mutagenesis primer 9eBamHIF
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<400> 81
qcattttaaga gatgggaccc gtctgccaca

30

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<210> 82
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
      oligonucleotide
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<220>
<221> misc_feature
<222> (1)..(30)
<223> Mutagenesis primer 9eBamHIR
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```
<400> 82
ctgtggcaga cgggtcccat ctcttaaattg
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30

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<210> 83
<211> 25
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
      oligonucleotide
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<220>
<221> misc_feature
<222> (1)..(25)
<223> Mutagenesis primer 732eNdeIF
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<400> 83
cgagatgcc a tacgtgaata cgcag

25

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<210> 84
<211> 25
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(25)
<223> mutagenesis primer 732eNde1R

<400> 84
ctgcgtattc acgtatggca tctcg

25

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<223> PCR primer 6-Nde1-M

<400> 85
ctgatatgcaa gtcatatgg ctcttctttc

30

<210> 86
<211> 34
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<213> Artificial Sequence

<220>
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oligonucleotide

<220>
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<222> (1)..(34)
<223> PCR primer 6-NdeI-R

<400> 86
gcccacgcgt ctcatatgag aatcagtaga tgcg

34

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
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Sequence

[illegible]

29

<213> Artificial Sequence

<223> Description of Artificial Sequence:
oligonucleotide

<223> PCR primer 8-NdeI-M

30

<213> Artificial Sequence

<223> Description of Artificial Sequence:
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<223> PCR primer 8-BamHI

29

<213> Artificial Sequence

<223> Description of Artificial Sequence:
oligonucleotide

<223> PCR primer 9-NdeI-M

30

<210> 91

<211> 34
<212> DNA
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<220>
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oligonucleotide

<220>
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<222> (1)..(34)
<223> PCR primer 9_BamHI

<400> 91
ggtcgactct agaggatcca ctagtgatat ggat

34

<210> 92
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oligonucleotide

<220>
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<222> (1)..(27)
<223> PCR primer 11-NdeI-M

<400> 92
gaacatatgg ctctcctttc tatcgta

27

<210> 93
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<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<222> (1)..(31)
<223> PCR primer 11-NdeI-R

<400> 93
ggtggtggtg tacatatgag acgcatacgg g

31

<210> 94
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(34)
<223> PCR primer 11-BamHI

<400> 94
gagactagac tggatcccat atacactgta atgg

34

<210> 95
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> PCR primer 2-NdeI-M

<400> 95
caaagggagc acatatggct ctgg

24

<210> 96
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(30)
<223> PCR primer 2-NdeI-R

<400> 96
ctgatgatgg tcatatgaga cgcataagtg

30

<210> 97
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(28)
<223> PCR primer 2-BamHI

<400> 97

11-BamHI
2-NdeI-M
2-NdeI-R
2-BamHI

28

<220>
<223> Description of Artificial Sequence:
oligonucleotide

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<400> 98
ccgatgatgg tcatatgaga cgcattgggcg
```

30

<220>
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oligonucleotide

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<220>  
<221> misc_feature  
<222> (1)..(30)  
<223> PCR primer 3-BamHI
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```
<400> 99
gggcatagat ttgagcggat cctacaaagg
```

30

```
<210> 100
<211> 24
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      oligonucleotide
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<222> (1)..(24)
<223> Mutagenesis primer 3elBamHIF
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<400> 100
cgtttgggaa tccatagaca tttc
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24

```
<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence
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Overall	Mean	1.00
	Standard Deviation	0.00
	Minimum	0.00
	Maximum	1.00
Group 1	Mean	1.00
	Standard Deviation	0.00
	Minimum	0.00
	Maximum	1.00
Group 2	Mean	1.00
	Standard Deviation	0.00
	Minimum	0.00
	Maximum	1.00
Group 3	Mean	1.00
	Standard Deviation	0.00
	Minimum	0.00
	Maximum	1.00
Group 4	Mean	1.00
	Standard Deviation	0.00
	Minimum	0.00
	Maximum	1.00

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(24)
<223> Mutagenesis primer 3e1BamHIR

<400> 101
gaaatgtcta tggattccca aacg

24

<210> 102
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(26)
<223> PCR primer 3e2BamHIF

<400> 102
gaagagatgg gaccgcgcct cgatag

26

<210> 103
<211> 26
<212> DNA
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oligonucleotide

<220>
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<222> (1)..(26)
<223> Mutagenesis primer 3e2BamHIR

<400> 103
ctatcgagga cgggtcccat ctcttc

26

<210> 104
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<222> (1)..(25)
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